

# Anti-cancer effects of artesunate in a panel of chemoresistant neuroblastoma cell lines

Michaelis, Martin; Kleinschmidt, Malte C.; Barth, Susanne; Rothweiler, Florian; Geiler, Janina; Breitling, Rainer; Mayer, Bernd; Deubzer, Hedwig; Witte, Olaf; Kreuter, Joerg

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**Table S1**

Correlation of gene expression with the artesunate IC50s determined in the cell lines UKF-NB-3, UKF-NB-3rVCR10, UKF-NB-3rCDDP1000, UKF-NB-6, UKF-NB-6rVCR10, and UKF-NB-6rCDDP1000 as indicated by Kendall's t-test.

Gene expression was determined by gene microarray analysis using Human Genome Survey Microarray V2.0 chips. Experiments were performed in triplicate.

Genes were selected from: Biochem Pharmacol 2002;64:617-23; Mol Pharmacol 2003;64:382-94; In Vivo 2005;19:225-32, Pharmacogenomics J 2006;6:269-78.

Genes that significantly (fdr < 0.05) correlate in their expression with artesunate IC50s are marked in bold.

correlation = direction of correlation between gene expression and artesunate IC50 as indicated by Kendall's t-test; (-) means inverse, (+) means positive

Ref_ART_correlation = direction of correlation as indicated in the literature

fdr_BF = false discovery rate determined using the Method of Bonferroni

p_greater = p-value for positive correlation

p_less = p-value for inverse correlation

tau = value for the extent of correlation (values can range from -1 to +1)

| Probe_ID | Gene_Symbol | Gene_Nam | Ref_ART_correlation | correlation | p_value | p_greater | p_less | tau |
|---|---|---|---|---|---|---|---|---|
| 210662 | ABCG1 | ATP-bindin | (-) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 210249 | ANAPC5 | anaphase p | (-) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 100039 | ANAPC7 | anaphase p | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 217383 | ANG | angiogenin | (-) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 115827 | AXL | AXL recept | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 200907 | BAG1 | BCL2-asso | (-) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 122149 | BAG3 | BCL2-asso | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 118877 | **BMP1** | bone morp | (-) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 186957 | BMPR2 | bone morp | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 158227 | **BRAF** | v-raf murin | (-) | (-) | **0,028** | 0,992 | **0,028** | -0,733 |
| 119580 | BRCA2 | breast can | (-) | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 211100 | CAT | catalase | (-) | (+) | 0,068 | 0,068 | 0,972 | 0,600 |
| 199852 | CCNL1 | cyclin L1 | (-) | (-) | 0,068 | 0,972 | 0,068 | -0,600 |
| 171254 | CDC25A | cell division | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 104054 | CDC42EP3 | CDC42 eff | (+) | (+) | 0,136 | 0,136 | 0,932 | 0,467 |
| 711223 | CDC42SE1 | CDC42 sm | (+) | (+) | 0,136 | 0,136 | 0,932 | 0,467 |
| 188843 | CDK8 | cyclin-depe | (-) | (-) | 0,068 | 0,972 | 0,068 | -0,600 |
| 191305 | CDKN3 | cyclin-depe | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 101377 | CIDEB | cell death-i | (-) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 141012 | COL18A1 | collagen, ty | (+) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 105493 | COL1A2 | collagen, ty | (+) | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 111306 | COL4A2 | collagen, ty | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 111068 | CSF1 | colony stim | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 204583 | CSK | c-src tyrosi | (-) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 154907 | CTGF | connective | (+) | (-) | 0,068 | 0,972 | 0,068 | -0,600 |
| 128477 | CXCL13 | chemokine | (+) | (-) | 0,068 | 0,972 | 0,068 | -0,600 |
| 166020 | CYR61 | cysteine-ric | (+) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 132884 | DHDH | dihydrodiol | (+) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 184324 | DNASE2 | deoxyribon | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 192173 | **DVL3** | dishevelled | (+) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 101210 | EFEMP1 | EGF-conta | (+) | (+) | 0,136 | 0,136 | 0,932 | 0,467 |
| 136952 | EGFR | epidermal g | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 198606 | EMP1 | epithelial m | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 196671 | EphA2 | EPH recep | (+) | (+/-) | 0,500 | 0,500 | 0,500 | 0,000 |
| 185249 | ERCC5 | excision re | (-) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 204787 | F3 | coagulation | (+) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 176815 | FEN1 | flap structu | (-) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 113042 | FGF2 | fibroblast g | (+) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 136386 | FN1 | fibronectin | (-) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 105390 | FOSB | FBJ murine | (+) | (+) | 0,136 | 0,136 | 0,932 | 0,467 |
| 117028 | FOSL2 | FOS-like a | (+) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 196828 | GCLC | glutamate-( | (+) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 145632 | GCLM | glutamate-( | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 202429 | GJA4 | gap junctio | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 100777 | **GSPT1** | G1 to S ph | (-) | (-) | **0,008** | 0,999 | **0,008** | -0,867 |
| 562311 | GSTA1 | glutathione | (+) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 170684 | GSTA2 | glutathione | (+) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 135910 | GSTM4 | glutathione | not available | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 214807 | GSTP1 | glutathione | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 133590 | GSTT2 | glutathione | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 158330 | GSTZ1 | glutathione | not available | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 138789 | HIF1A | hypoxia-ind | (+) | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 103694 | HMGB1 | high-mobili | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 171265 | HMGN2 | high-mobili | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 137986 | IL13RA1 | interleukin | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 115545 | IL6ST | interleukin | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 187921 | **IRF4** | interferon r | (-) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 111199 | KIF5B | kinesin fam | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 180804 | LIG1 | ligase I, DN | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 176287 | MADD | MAP-kinas | (-) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 131781 | **MEN1** | multiple en | (-) | (+) | **0,028** | **0,028** | 0,992 | 0,733 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 137942 | MGST1 | microsoma | (+) | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 177655 | MGST3 | microsoma | (+) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 135420 | MMP11 | matrix meta | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 112640 | MMP9 | matrix meta | (-) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 161318 | MPDZ | multiple PD | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 110763 | MPHOSPH10 | M-phase pl | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 217047 | MPHOSPH6 | M-phase pl | (-) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 200184 | MYB | v-myb mye | (-) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 132666 | MYC | v-myc mye | (-) | (+/-) | 0,500 | 0,500 | 0,500 | 0,000 |
| 108491 | NID2 | nidogen 2 ( | (+) | (+) | 0,068 | 0,068 | 0,972 | 0,600 |
| 124833 | NOS2A | nitric oxide | (-) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 106462 | NRCAM | neuronal ce | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 130678 | PA2G4 | proliferatio | (-) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 218609 | PDCD2 | programme | (-) | (+/-) | 0,500 | 0,500 | 0,500 | 0,000 |
| 208672 | **PLAU** | plasminoge | (+) | (+) | **0,028** | **0,028** | 0,992 | 0,733 |
| 158513 | PRDX2 | peroxiredox | not available | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 215425 | PRDX6 | peroxiredox | not available | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 190571 | RAB2 | RAB2, mer | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 140316 | RAN | RAN, mem | (-) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 199683 | RHOC | ras homolo | (+) | (+) | 0,235 | 0,235 | 0,864 | 0,333 |
| 129829 | RND3 | Rho family | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |
| 215633 | RPS3 | ribosomal p | (-) | (+/-) | 0,500 | 0,500 | 0,500 | 0,000 |
| 144600 | TFPI2 | tissue facto | (+) | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 158090 | TGFB2 | transformin | (+) | (-) | 0,360 | 0,765 | 0,360 | -0,200 |
| 162911 | THBS1 | thrombospo | (+) | (-) | 0,500 | 0,640 | 0,500 | -0,067 |
| 179728 | TOP1 | topoisomer | (+) | (+) | 0,500 | 0,500 | 0,640 | 0,067 |
| 116930 | TOP2B | topoisomer | not available | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 164267 | TUBB4 | tubulin, bet | (+) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 164857 | TXNRD1 | thioredoxin | (+) | (-) | 0,136 | 0,932 | 0,136 | -0,467 |
| 136294 | TXNRD2 | thioredoxin | (+) | (+) | 0,136 | 0,136 | 0,932 | 0,467 |
| 193721 | **UBE2A** | ubiquitin-co | (+) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 204651 | UNG | uracil-DNA | (-) | (-) | 0,235 | 0,864 | 0,235 | -0,333 |
| 170337 | VEGFC | vascular en | (+) | (+) | 0,360 | 0,360 | 0,765 | 0,200 |

Table S1 significant genes_1

| Probe_ID | Gene_Sym | Gene_Nam | Ref_ART_( | correlation | p_value | p_greater | p_less | tau |
|---|---|---|---|---|---|---|---|---|
| 118877 | **BMP1** | bone morp | (-) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 158227 | **BRAF** | v-raf murin | (-) | (-) | **0,028** | 0,992 | **0,028** | -0,733 |
| 192173 | **DVL3** | dishevelled | (+) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 100777 | **GSPT1** | G1 to S ph | (-) | (-) | **0,008** | 0,999 | **0,008** | -0,867 |
| 187921 | **IRF4** | interferon r | (-) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |
| 131781 | **MEN1** | multiple en | (-) | (+) | **0,028** | **0,028** | 0,992 | 0,733 |
| 208672 | **PLAU** | plasminoge | (+) | (+) | **0,028** | **0,028** | 0,992 | 0,733 |
| 193721 | **UBE2A** | ubiquitin-co | (+) | (+) | **0,008** | **0,008** | 0,999 | 0,867 |